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750-1000 Summary 5

Symbiosis

Words: 844

Belcaid, M., Casaburi, G., McAnulty, S. J., Schmidbaur, H., Suria, A. M., Moriano-Gutierrez, S., ... & Collins, A. J. (2019). Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. *Proceedings of the National Academy of Sciences*, 201817322.

Hansen, A. K., & Moran, N. A. (2011). Aphid genome expression reveals host–symbiont cooperation in the production of amino acids. *Proceedings of the National Academy of Sciences*, *108*(7), 2849-2854.

In this summary, I will define and describe symbiotic relationships as well as discuss its impact on evaluating physiological performance of an organism. I will then compare two scientific studies that focused on explaining these symbiotic relationships in cephalopods and aphids using genomic analysis.

Symbiosis refers to a functioning relationship between two organisms, often beneficial to both parties involved. There are three forms of a symbiotic relationship: mutualism, parasitism, and commensalism. Mutualism describes a relationship where both partners benefit from the interaction, which includes coral and its symbionts. A parasitic relationship involves one partner benefiting at the expense of the other, which includes parasitic worms and their hosts. Commensalism refers to a relationship where one partner benefits and the other is unaffected, which includes remora fish and its host, a shark. A complex symbiotic relationship like the coral holobiont, consists of three partners: the coral host, its symbionts, and the surrounding microbiome. The symbionts and microbiome play a key role in the overall physiology and performance of the coral holobiont. Each partner in the holobiont struggles to survive without the others. When investigating the effects of climate change or the evolution of these species, looking at the holobiont compared to solely looking at the coral host becomes increasingly important. Only focusing on one organism in the symbiotic relationship will not produce a holistic view or conclusion. The interactions between organisms are often complex and require integrative research to elucidate the functional relationship between the two or more organisms.

Belcaid and team investigated host-microbe interactions in the light organ and a reproductive organ in the cephalopod, *Euprymna* *scolopes*. Their results suggest that how these two symbiotic organs evolved and the mechanisms underlying that evolution are different. The microbiome associated with each organ has been identified, but the research team focused on the origin and how these differing symbiotic relationships within a single host evolved. Genome sequences were available for this model organism and for a similar cephalopod that did not have these symbiotic organs, creating an ideal situation for comparison. This study presents the first genome assembly for this particular suborder, and most detailed for a cephalopod.  The team used a combination of sequencing techniques to assemble and annotate this genome, including RNA seq and ISO-seq to create transcriptomic libraries. After sequencing, the team was able to compare the genomes of the octopus and bobtail squid to find a substantial difference in genome size, which they attributed to differences in long interspersed nuclear elements (LINEs) between the two organisms. Their results also suggest there was a genomic reorganization in a common cephalopod ancestor because they observed local gene linkages that had been disrupted. The two organisms contained large intergenic distance differences in *hox* gene clusters that could be contributing to the evolution of unique organs. There was evidence of gene duplication in the light and reproductive organs of the bobtail squid that is specific to the bobtail squid and absent in the cephalopod. Within the reproductive (ANG) organ, there was a large proportion (35%) of *E. scolopes*-specific genes, referred to as orphan genes. In conclusion, the authors identified the increase in LINEs as a potential precursor for new function because this allowed a unique genome architecture. Because the ANG organ contains taxon-specific (orphan) genes, the authors suggest it is highly derived and evolved by different mechanisms than the light organ.

Hansen and team investigated the symbiotic relationship between a bacterial endosymbiont and aphids, and how the partnership is able to supply all the nutrients and amino acids needed for processes like amino acid biosynthesis despite a lack of genes in essential amino acid pathways in the bacteria. Similarly to Belcaid, Hansen used RNA seq and pathway analysis to look at (1) if the bacterial and host genomes coordinate to produce essential amino acid, (2) the potential dependence on the host by the bacteria for nonessential amino acids, and (3) how the organism obtains nitrogen for amino acid production. Their results indicate that the host and bacterial genomes work together to produce the necessary amino acids and that the supply for nitrogen is the GOGAT cycle. Transcriptional analysis supports the idea that the aphid supplies the function from genes that the bacteria is lacking. In some ways, the host is able to finish the job that the bacteria started for essential amino acids. However, for biosynthesis of non-amino acids, the bacteria is dependent on the host. Regarding the production of nitrogen, the team found upregulation in genes that encode for enzymes that recycle ammonia into amino acids. This supports the idea that the bacteria depend on the host for the nitrogen needed during amino acid production.

These two papers illustrate how complex the symbiotic relationships can be across all environments and organisms. Although not impossible to tease apart, the complexity of these organisms creates difficulties when attempting to assess characteristics like physiological tolerance and evolution. The boom in number and quality of genomic techniques is allowing all fields to dive further into these relationships to better understand the origin, evolutionary mechanisms, and function of the symbiosis.